Identification of selection signatures using homozygous regions in the turkey (*Meleagris gallopavo*) genome

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Background

- As a result of artificial or natural selection, "selection signatures", or specific patterns of variation can be identified along the genome
- Contiguous sequences of homozygous genotypes (runs of homozygosity, ROH) can be used to help identify selection signatures
- Inference about functional characteristics of these regions may help to better understand positive or negative pleiotropic effects and/or genetic hitch-hiking with alleles under selection

Objectives

1. **Determine genomic inbreeding based on ROH (F_{ROH}) and distribution of ROH on turkey autosomes in three different breeding lines**
2. **Identify selection signatures**

Materials and Methods

Line A	Line B	Line C
1,082 birds	1,297 birds	1,663 birds
53,815 SNPs	52,199 SNPs	52,807 SNPs

ROH detected using R package "detectRUNS"
- Minimum 50 SNP and 1Mb in length
- No missing or opposite genotypes
- Maximum gap between consecutive SNP: 1Mb

Impact on the Industry

- Gain a better understanding of population history and genetic mechanisms affecting phenotypic differentiation in turkeys
- Information gained regarding variants in turkey lines is important for genetic studies involving association analyses with relevant phenotypes
- Genes detected in regions of putative selection can aid in further improvement of economically important traits
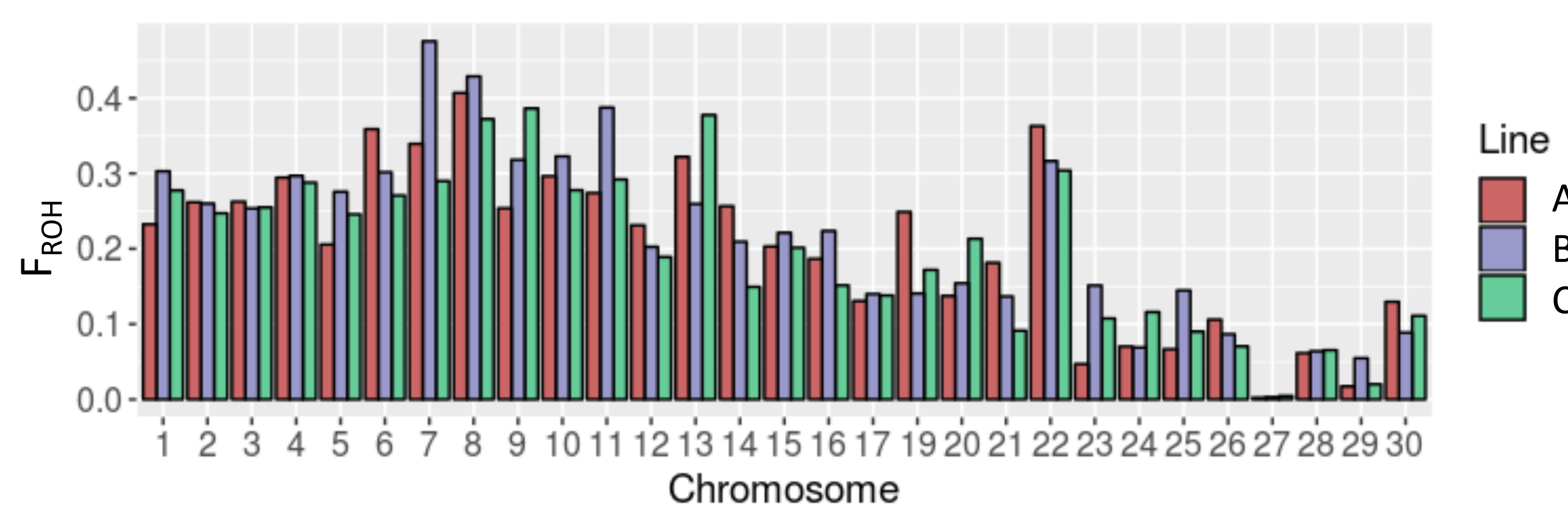
Results

Figure 1. Average F_{ROH} per chromosome along turkey autosomes with average F_{ROH}, genome-wide, of 0.21, 0.22, and 0.20 for lines A, B, and C, respectively.
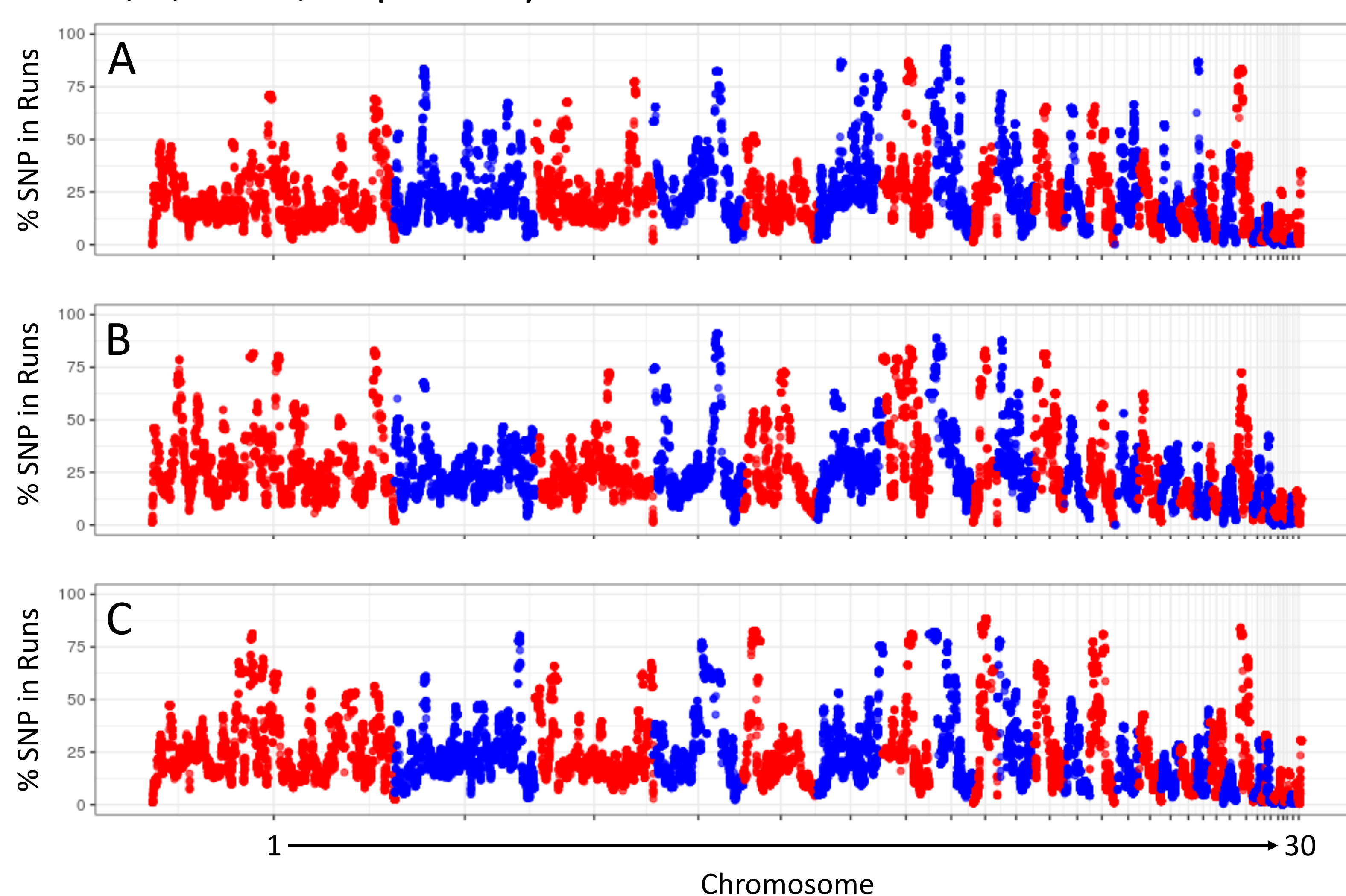

Figure 2. Manhattan plots for percentage of animals that share a SNP that falls within a ROH with respect to the position along the genome.
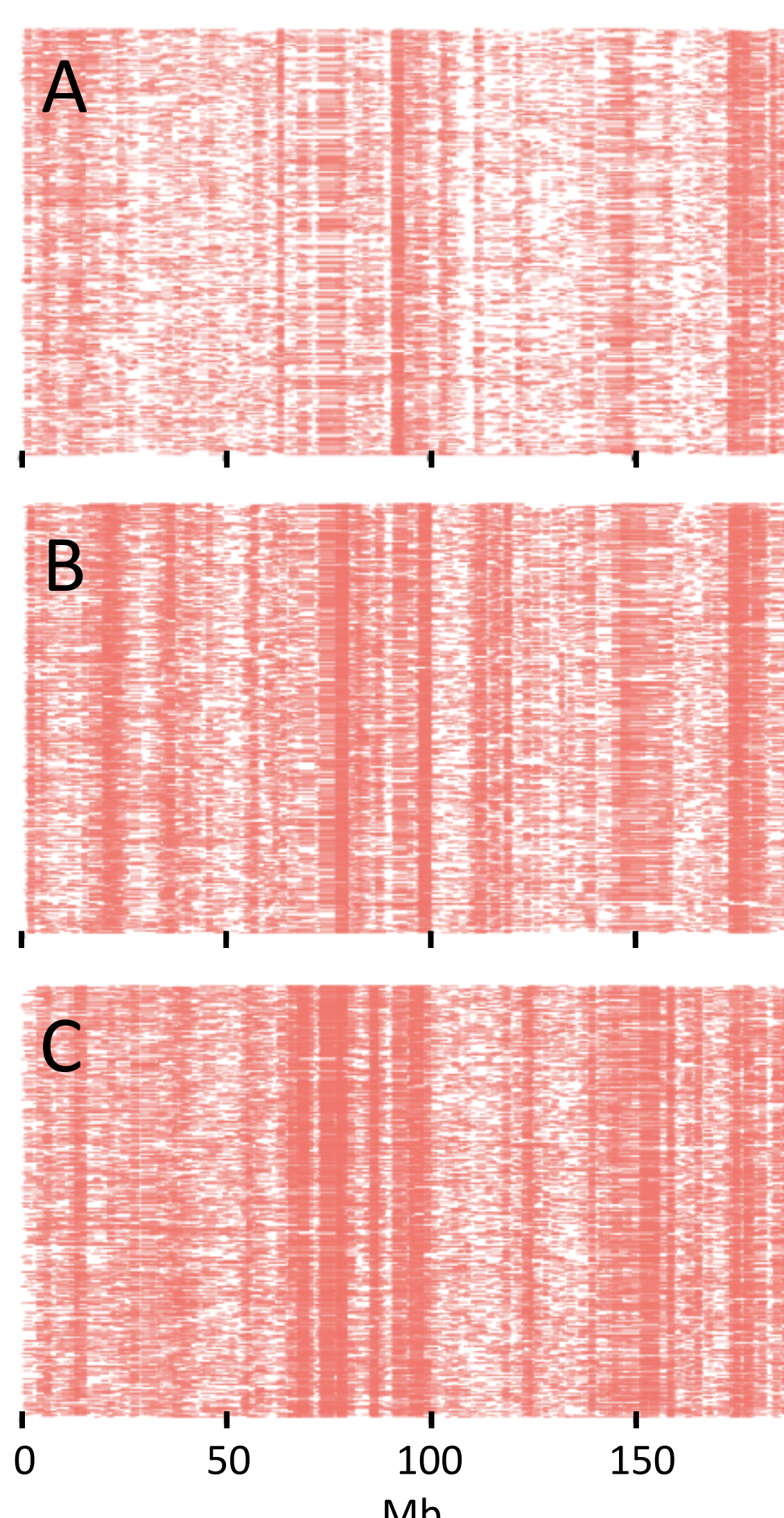

Figure 3. ROH on chromosome 1 for lines A, B, and C; individual IDs on the y-axis and base pairs on the x-axis.

Conclusions

- Average F_{ROH} per chromosome varies between lines and chromosomes
- Line-specific and common ROH detected across genome

Future Steps

- Estimate fixation index (F_{ST}) and integrated haplotype score (iHS) to complement detection of ROH in order to more accurately identify selection signatures
- Annotate candidate regions to identify genes associated with economically important traits